AMENDMENT TO THE SPECIFICATION

Please replace the paragraph beginning on page 5, line 14 with the following:

Fig. 1. Positional cloning of the *SOS1* gene. (A) Physical mapping of *SOS1*. All the SSLP markers shown except ngal 145 were developed in this study based on sequence information of the bacterial artificial chromosomes (BACs). The BAC contig was assembled based on information available at ~~http://www.Arabidopsis.org/cgi-bin/maps,~~ publicly available databases, which are incorporated herein by reference. (B) Structure of the *SOS1* gene. Positions are relative to the initiation codon. Filled boxes indicate the open reading frame and lines between boxes indicate introns.

Please replace the paragraph beginning on page 5, line 27 with the following:

Fig. 3. *SOS1* is predicted to encode a transmembrane protein. (A) The deduced amino acid sequence of *SOS1* (SEQ ID NO:2). The 12 putative transmembrane domains (TM) are underlined. (B) Hydrophobicity plot of *SOS1*. The hydrophobicity values were calculated by the program Tmpred available at ~~http://www.ch.embnet.org/software/TMPRED_form.html, incorporated herein by reference~~ publicly available sources.

Please replace the paragraph beginning on page 6, line 1 with the following:

Fig. 4. *SOS1*, is similar to Na^+/H^+ antiporters. (A) Alignment of *SOS1* SEQ ID NO:2 (accession number AF256224) with Na^+/H^+ antiporters NHE1 from Chinese hamster SEQ ID NO:3 (P48761) and NhaP from *Pseudomonas aeruginosa* SEQ ID NO:4 (BAA31695). The sequences were aligned by the program ClustalW ~~(http://dot.imgen.bcm.tmc.edu:9331/multi-align/Options/clustalw.html, incorporated herein by reference)~~. Amino acids identical in at

least two proteins are highlighted in black and conservative substitutions in grey. * indicates conserved residues that were substituted in *sos1* mutant alleles. (B) Phylogenetic analysis of *SOS1* and other representative Na^+/H^+ antiporters. Multiple sequence alignment was performed with ClustalW. The alignment is based on the N-terminal 450 amino acids of *SOS1*. Evolutionary distances were calculated by the Neighbor Joining method and the phylogenetic tree was drawn by the program Drawgram ~~(http://bioweb.pasteur.fr/seqanal/phylogeny/phylip-uk.html, incorporated herein by reference)~~. The accession number and source of each of the other representative Na^+/H^+ antiporters are as follows: NHE1 (P19634), *Homo sapiens*; NHE2 (AAD41635), *Homo sapiens*; NHE3 (P48764), *Homo sapiens*; NHE4 (P26434), *Rattus norvegicus*; NIBS (AAC98696.1), *Homo sapiens*; NHE6 (NP_006350), *Homo sapiens*; NHA1 (NP_013239), *Saccharomyces cerevisiae*; NHX1 (NP 010744), *Saccharomyces cerevisiae*; AtNHXl (AAD16946.1), *Arabidopsis thaliana*; SOD2 (CAA77796.1), *Schizosaccharomyces pombe*; NhaA (P13738), *Escherichia coli*; NhaP (BAA31695.1), *Pseudomonas aeruginosa*.

Please replace the paragraph beginning on page 6, line 30 with the following:

Fig. 7. Nucleotide sequence of the SOS1 gene, SEQ ID NO:1 (Genbank accession number AF256224). Fig. 7A shows nucleotides 1-1980 of SEQ ID NO:1, Fig. 7B shows nucleotides 1981-4020 of SEQ ID NO:1, Fig. 7C shows nucleotides 4021-6060 of SEQ ID NO:1, and Fig. 7D shows nucleotides 6061-6076 of SEQ ID NO:1.

Please replace the paragraph beginning on page 13, line 11 with the following:

T20F6-1-F: 5'-GGATGATGATCGATTCGGAT-3' (SEQ ID NO:5)

T20F6-1-R: 5'-ATCTGACTCATAGGATATCG-3' (SEQ ID NO:6)

ngal 145-F: 5'-CCTTCACATCCAAAACCCAC-3' (SEQ ID NO:7)

ngal 145-R: 5'-GCACATACCCACAACCAGAA-3' (SEQ ID NO:8)

F5O4-3-F: 5'-GAATGTTTTGAAGGATATCTCAG-3' (SEQ ID NO:9)

F5O4-3-R: 5'-GAAAAATGGAGCACGAAATAAGC-3' (SEQ ID NO:10)

F14H20-3-F: 5'-CCCGAGATTAATACACAATC-3' (SEQ ID NO:11)

F14H20-3-R: 5'-GCAGATTATGTAATTGTGACC-3' (SEQ ID NO:12)

T23K3-1-F: 5'-TCGTGTTTACCGGGTCGGAT-3' (SEQ ID NO:13)

T23K3-1-R: 5'-TGATGAGAATCTTAGCGAGC-3' (SEQ ID NO:14)

CCC-1-F: 5'-TGGTAAGACCAAATTACACTC-3' (SEQ ID NO:15)

CCC-I-R: 5'-CGTAATTAAAATGTGTTAAACCG-3' (SEQ ID NO:16)

F10A8-1-F: 5'-AACCGCATAGTACAATGCAG-3' (SEQ ID NO:17)

F10A8-1-R: 5'-CGGTAAAGATCAACTAATAACG-3' (SEQ ID NO:18)

F23H14-3-F: 5'-AACGGAAACGGCAACTAGAC-3' (SEQ ID NO:19)

F23H14-3-R: 5'-ACCCTAAATGTTTCGATTCG-3' (SEQ ID NO:20)

Please replace the paragraph beginning on page 17, line 29 with the following:

To determine whether NaCl up-regulation of *SOS1* is under control of the SOS3/SOS2 regulatory pathway, ~~SOS}~~ *SOS1* expression in *sos2*-l and *sos3*-1 mutant plants was analyzed. In the *sos2* mutant. *SOS1* was up-regulated by NaCl stress in the root but not in the shoot (Fig. 6C). In *sos3* plants, no *SOS1* up-regulation was seen in either the root or shoot (Fig. 6D). These results show that *SOS1* expression is regulated at least in part by the SOS3/SOS2 pathway.

Please replace the paragraph beginning on page 19, line 22 with the following:

SOS1 is essential for the homeostasis of both $Na^+$and K^+. Under NaCl stress, *sos1* mutant plants accumulate less Na^+ as well as less ~~W~~ $\underline{K^+}$ (11, 31). *SOS1* gene expression is concentrated in cells surrounding the xylem, suggesting that *SOS1* may function in loading Na^+ into the xylem for long distance transport (our unpublished data). A xylem loading function of *SOS1* would be consistent with *sos1* mutant plants accumulating less Na^+. Preferential expression of *SOS1* at the symplast/xylem boundary would also help explain the K^+ transport defect of *sos1* mutant plants. It is well known that H^+ and Na^+ transport is closely linked at the xylem/symplast interface (32). The effect of *SOS1* on K^+ transport might be through its effect on ~~W~~ $\underline{H^+}$ gradient across the cell membrane of stellar cells. For example, a K^+-H^+ symporter activity could be coupled with *SOS1* via H^+ cycling and such a symporter may be required for high affinity ~~W~~ $\underline{K^+}$ transport into the xylem. It is also possible that a K^+/Na^+ symporter is coupled with *SOS1* via Na^+ cycling.